

GenCore version 5.1.4-p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2003, 21:53:16 ; Search time 1362 seconds

(without alignments)  
5755.224 Million cell updates/sec

Title: US-09-750-456-393

Perfect score: 484

Sequence: 1 us-09-750-456-393

Scoring table: IDENTITY\_NUC

Searched: 16154066 seqs, 8037743376 residues

Total number of hits satisfying chosen parameters: 31308134

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pla:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	407	84.1	836	14	BM944452 UI-M-EHQP
2	195.4	40.4	759	9	AU079894 AU079894
3	181.4	37.5	604	14	BM950073 UI-M-EHQP
4	143.8	29.7	700	9	AU067452 AU067452
5	132.8	27.4	744	10	BB632601 BB632601
6	131.4	27.1	752	13	CNS04452 CNS04452

7	129.4	26.7	802	17	CNS04SMG	AL055377 Tetradon
8	128	26.4	504	13	B1882735	B1882735 fmg7409.x
9	117.8	24.3	335	17	CNS030BT	AL022050 Tetradon
10	108.5	22.5	551	12	B3739443	B3739443 fmg7409.y
11	105	21.7	1054	17	CNS030CQ	AL179522 Tetradon
12	103	21.3	436	9	AA663739	AA663739 ae71d04.s
13	93.2	19.3	405	10	AW482601	AW482601 46248.MAR
14	86.4	17.9	655	13	BM494257	BM494257 IP0GBR1_1
15	81.4	16.8	952	17	CNS030HW	AL199149 Tetradon
16	80.6	16.7	978	12	PE70254	PE70254 2V7.NM102
17	73.8	15.2	324	10	AW353965	AW353965 32999.MAR
18	71.8	14.8	831	17	CNS04YR2	AL120602 Tetradon
19	70.4	14.5	329	10	B2131102	B2131102 PR131102
20	69.9	14.4	722	17	CNS047VY	AL127802 Tetradon
21	65.6	13.6	1200	17	CNS06EXM	AL134207 Tetradon
22	63.8	13.2	898	12	BE528267	BFE08907 fmg7409.z
23	60.4	12.5	615	13	BM537155	BM537155 h378005.g
24	59.8	12.4	929	17	CNS043Y4	AL041172 Tetradon
25	57.6	11.5	759	9	AU066842	AU066842 AU066842
26	50.2	10.4	79	14	PA6242	PA6242 y043409.r1
27	47.6	9.8	925	17	CNS030IF	AL053012 Drosophila
28	47.4	9.8	910	17	CNS030IF	AL065629 Drosophila
29	46	9.5	513	12	B3913141	B3913141 fmg7409.a05
30	45.8	9.5	559	13	BM426407	BM426407 p9f2n.pkc
31	45.8	9.5	591	13	BM489046	BM489046 p9m2n.pkc
32	45.9	9.5	629	13	BM491559	BM491559 f9p2n.pkc
33	45.2	9.3	848	17	AC036341	AG036341 Pan trogl
34	44.4	9.2	925	17	CNS030IF	AL053012 Drosophila
35	42.8	8.9	300	10	BE389767	PR188767 PR188767
36	41.2	8.5	598	13	BM077103	BM077103 TREST-A30
37	40.8	8.4	645	17	CNS01213	AL101589 Drosophila
38	40.6	8.4	1201	17	CNS015XQ	AL106040 Drosophila
39	40.2	8.3	1101	17	CNS001XT	AL078875 Drosophila
40	39.8	8.2	912	17	AG153593	AG153593 Pan trogl
41	39.6	8.2	586	12	BP440154	BP440154 fmg7409.b02
42	39.4	8.1	1009	17	CNS010PW	AL068882 Drosophila
43	39.2	8.1	322	14	B2895473	B2895473 AGFM09RT
44	39	8.1	977	17	CNS030CQ	AL077645 Tetradon
45	38.8	8.0	708	12	B9833700	B9833700 EST0001.H

#### ALIGNMENTS

RESULT 1  
LOCUS BM944452  
DEFINITION UI-M-EHQP-bv1-1-02 C UI-M-EHQP\_EHQP\_Mus musculus cDNA clone  
IMAGE:5695945 5', mRNA sequence.  
ACCESSION BM944452  
VERSION BM944452 1 GI:19428037  
KEYWORDS PST  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 826)  
AUTHORS NIH MGC <http://mgc.ncbi.nlm.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Dr. James Jiri, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
RNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E Consortium/MIAMI at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pVX-5  
Location/Qualifiers

FEATURES

1. .826  
/organism="Mus musculus"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5445041"  
/clone\_id="NIMH\_BMAP\_EH0P"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 18.5 dpc"  
/lab\_host="PHAGE (T1 phage resistant)"  
/note="Clonal brain, vector: pX-852, Site 1, Ecol I, Site 2; Not I. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:741-805, 1994. Purified mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo. It filter containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGGAGAGAG. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

	84.18	Score 407	SE 14	Length 926
Every Match				
Best Local Similarity	36.28	Prod. No. 1.1e 98		
Matthew 422, Conservative	0	Mismatches 15	Indels 2	Gaps 2

[illegible]

0y 130 CTAGTGTATTTTATAGAACTTTCTTATATATGATATATTTATATATTTCTGAGGAC 189

**PY**      100-THATTAAGGTTTAAAGAATTCTTCGTGAACG    249

Db 559 135C1GAGGCTGAGGGGCTGTTGAGGCTGTTTCTTCTGTTCTGGGAAACCCCGAAGC 618

619 AATTGCTTGTATTTGTAAGACGGGCAACTGTGTAAAGAGCGTCATTTC 678

310 1CTTGAATGATGGAACCGGTTTCTGTCGTCGCGCTCTGAGACAGAGAGGTCACGCGTCT 369

[illegible]

Db 738 TAATTATGACCTTCATGTACATGAANATCAAGTGTGCACTTGGGATTCGCAATGGACACGGAAAG 797

[illegible]

AU079894  
L. 10000  
A. 10000  
2500  
10000  
10000  
10000

5', mRNA sequence.  
ACCESSION AD079894

**KEYWORDS:** EST; Income Tax; Corporate Tax

ORGANISM	REFERENCE	TITLE	COMMENT
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus			
1 (Accession 759)			
Hashimoto, Y., Tsubota, T., Tanuma, F., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.			
Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method			
unpublished (1999)			
Genbank, Fatsuyuki Hashimoto			
Division of Genetic Resources			
National Institute of Infectious Diseases			
43-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan			
Email: khashim@nig.go.jp			
URL: <a href="http://www.nig.go.jp/genet/jp-start/">http://www.nig.go.jp/genet/jp-start/</a>			
Location/Qualifiers			

FFA#TYPE	LOCATION/Qualifiers
SOURCE	1. 759

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/strain="C57BL"
/ob_xref="axon.10090"
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/clone_lib="Sugano mouse brain mcb"
/sex="Female"

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lab_pos = "top10"
model = program_baird_van_der_Weide_1998_ELB_1st_stage_GDPA

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The following sequence was used as a double-stranded cDNA template for a blunt-ended PCR reaction (see below), digested at

sites just outside the Drail sites can be used to isolate the other itself. Sites adjacent to the Drail sites

at (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing: 5' end primer

[illegible]

ORIGIN

Test Local Similarity 55.4%; Pct 1 NO. 5.3e-38;  
Matches 310; Conservative 0; Mismatches 160; Indels 4; Gaps 3

[illegible]

71 GGGGGAAGAACTGTATTTTGGTAAATTGAGAATAAGCTGTCTCTCGGGGCTGGCC 130

DY

Db 232 AATAAG 32135511AATCTCTCTTAATTAAGAGTCTGGAATGCTATAGGCG 288

289 TACCTGCGCTGACGCGGCACTATTATTATGAGGAGAGTAAAGAT 347

191 00010A30020A30030A30040A30050A30060A30070A30080A30090A30100A30110A30120A30130A30140A30150A30160A30170A30180A30190A30200A30210A30220A30230A30240A30250A30260A30270A30280A30290A30300A30310A30320A30330A30340A30350A30360A30370A30380A30390A30400A30410A30420A30430A30440A30450A30460A30470A30480A30490A30500A30510A30520A30530A30540A30550A30560A30570A30580A30590A30600A30610A30620A30630A30640A30650A30660A30670A30680A30690A30700A30710A30720A30730A30740A30750A30760A30770A30780A30790A30800A30810A30820A30830A30840A30850A30860A30870A30880A30890A30900A30910A30920A30930A30940A30950A30960A30970A30980A30990A31000A31010A31020A31030A31040A31050A31060A31070A31080A31090A31100A31110A31120A31130A31140A31150A31160A31170A31180A31190A31200A31210A31220A31230A31240A31250A31260A31270A31280A31290A31300A31310A31320A31330A31340A31350A31360A31370A31380A31390A31400A31410A31420A31430A31440A31450A31460A31470A31480A31490A31500A31510A31520A31530A31540A31550A31560A31570A31580A31590A31600A31610A31620A31630A31640A31650A31660A31670A31680A31690A31700A31710A31720A31730A31740A31750A31760A31770A31780A31790A31800A31810A31820A31830A31840A31850A31860A31870A31880A31890A31900A31910A31920A31930A31940A31950A31960A31970A31980A31990A32000A32010A32020A32030A32040A32050A32060A32070A32080A32090A32100A32110A32120A32130A32140A32150A32160A32170A32180A32190A32200A32210A32220A32230A32240A32250A32260A32270A32280A32290A32300A32310A32320A32330A32340A32350A32360A32370A32380A32390A32400A32410A32420A32430A32440A32450A32460A32470A32480A32490A32500A32510A32520A32530A32540A32550A32560A32570A32580A32590A32600A32610A32620A32630A32640A32650A32660A32670A32680A32690A32700A32710A32720A32730A32740A32750A32760A32770A32780A32790A32800A32810A32820A32830A32840A32850A32860A32870A32880A32890A32900A32910A32920A32930A32940A32950A32960A32970A32980A32990A33000A33010A33020A33030A33040A33050A33060A33070A33080A33090A33100A33110A33120A33130A33140A33150A33160A33170A33180A33190A33200A33210A33220A33230A33240A33250A33260A33270A33280A33290A33300A33310A33320A33330A33340A33350A33360A33370A33380A33390A33400A33410A33420A33430A33440A33450A33460A33470A33480A33490A33500A33510A33520A33530A33540A33550A33560A33570A33580A33590A33600A33610A33620A33630A33640A33650A33660A33670A33680A33690A33700A33710A33720A33730A33740A33750A33760A33770A33780A33790A33800A33810A33820A33830A33840A33850A33860A33870A33880A33890A33900A33910A33920A33930A33940A33950A33960A33970A33980A33990A34000A34010A34020A34030A34040A34050A34060A34070A34080A34090A34100A34110A34120A34130A34140A34150A34160A34170A34180A34190A34200A34210A34220A34230A34240A34250A34260A34270A34280A34290A34300A34310A34320A34330A34340A34350A34360A34370A34380A34390A34400A34410A34420A34430A34440A34450A34460A34470A34480A34490A34500A34510A34520A34530A34540A34550A34560A34570A34580A34590A34600A34610A34620A34630A34640A34650A34660A34670A34680A34690A34700A34710A34720A34730A34740A34750A34760A34770A34780A34790A34800A34810A34820A34830A34840A34850A34860A34870A34880A34890A34900A34910A34920A34930A34940A34950A34960A34970A34980A34990A35000A35010A35020A35030A35040A35050A35060A35070A35080A35090A35100A35110A35120A35130A35140A35150A35160A35170A35180A35190A35200A35210A35220A35230A35240A35250A35260A35270A35280A35290A35300A35310A35320A35330A35340A35350A35360A35370A35380A35390A35400A35410A35420A35430A35440A35450A35460A35470A35480A35490A35500A35510A35520A35530A35540A35550A35560A35570A35580A35590A35600A35610A35620A35630A35640A35650A35660A35670A35680A35690A35700A35710A35720A35730A35740A35750A35760A35770A35780A35790A35800A35810A35820A35830A35840A35850A35860A35870A35880A35890A35900A35910A35920A35930A35940A35950A35960A35970A35980A35990A36000A36010A36020A36030A36040A36050A36060A36070A36080A36090A36100A36110A36120A36130A36140A36150A36160A36170A36180A36190A36200A36210A36220A36230A36240A36250A36260A36270A36280A36290A36300A36310A36320A36330A36340A36350A36360A36370A36380A36390A36400A36410A36420A36430A36440A36450A36460A36470A36480A36490A36500A36510A36520A36530A36540A36550A36560A36570A36580A36590A36600A36610A36620A36630A36640A36650A36660A36670A36680A36690A36700A36710A36720A36730A36740A36750A36760A36770A36780A36790A36800A36810A3682

251 GTGTGGTGGGTTTATTNAAATATATGTGAGAGGCGTGGAAATGGTGGT 310

Db 408 GTGGCTTAGAATTCTGAAAAAATAATGATGAGATGGATACGATACGTT 467

[illegible]

430 AACGATGAGGCTGATGACATGAAATATAGTGGTATTTGGATGACAGGGAGG 430

[illegible]







[illegible]

REFERENCE		Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
ATTNORS		1 (bases 1 to 802)
TITLE		Poest-Crollius,H., Jalllon,O., Dasilva,C., Rouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence
JOURNAL REFERENCE		Unpublished 2 (bases 1 to 902) Poest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Rouneau,L., Rillaudt,A., Querier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE		Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL REFERENCE		Unpublished 1 (bases 1 to 802) Genoscope.
AUTHORS		Direct Submission Submitted (12-Apr-2000)
TITLE		This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .
COMMENT		Location/Qualifiers
FEATURES		1..802 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="007D16" /clone_1ib="H" /note="Genoscope sequence ID : CORH007PB08XD1-end : T7"
SOURCE		185 a 136 c 213 j 200 t ? others
CPIGIN		
Query Match	26.7%	Score 129.4; DB 17; Length 802;
Post local similarity	66.0%	Frd 30 98.22;
Matches	214; Conservative	1; Mismatches 105; Indels 4; Gaps 2;
QY	7	TTGCCCCAGACAGAGCGAGGTCTCTGGACTGGAGATGAGCTGTACTCTCCCTGCTTCGC 66
DB	237	TTGCCCCAGAGAGAGAGATTTGAATTTGAACAGAGAAATTAATTAATTAAGATTTGCT 246
QY	67	GAG 126
DB	297	GAG 353
QY	127	TGGCTAAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 186
DB	354	CAGCTATATGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 413
QY	187	GAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 246
DB	414	GAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 472
QY	247	AGCAGTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 306
DB	473	AGCAGTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 512
QY	307	TGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 330
DB	533	ACATATGCCAGCTGCACCGGCACCG 556
RESULT 8		
LOCUS	B1882735	504 bp MPNA 11base EST 12 OCT 2001
DEFINITION	fm07309 x1 zehrafish Research Genomics CDS full length cDNA	
VERSION	1.0	
KEYWORDS	EST.	
SCUPCE	zefrafish.	





[illegible]

RESULT 12	AA63737.0	LOCUS	DEFINITION
AA653733	435 bp	GENA	EST 15-DEC-1997
de/11441st	Stratagene	SCHLZ brain	211 Homo sapiens cDNA clone
IMAGE:099607	3' similar to	TR0305716	0305716 NEUREXIN II ALPHA A
PRECURSOR	1	MPNA	sequence

ACCESSION	AB063733
VERSION	1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE  
AUTHORS  
1 (bases 1 to 436)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE  
 JOURNAL  
 WASHU-NCI human EST Project  
 Unpublished (1997)  
 COMMENT  
 Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through EMBL. Contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Possible reversed orientation similarity of writing strand  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 356.

FEATURES	Location/Qualifiers
Source	1. .436

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cclone="IMAGE:56267"  
 /cclone\_id="Stratagene schizo brain 511"  
 /sex="male"  
 /tissue\_type="schizophrenic brain S-11 frontal lobe"  
 /dev\_stage="34 years old"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Vector: Bluescript SK, site 1 EcoRI, library  
 constructed from S-11 frontal lobe, male, 34 years old,  
 50% Caucasian, 50% Aleutian, schizophrenic, suicide.  
 Random primed into EcoRI site of ZAP II Vector. Mass  
 excised. Custom library. Avg insert length 1.4kb.  
 Material obtained by Johnston N., Torrey, E.F., Yolken R.,  
 and the Stanley Neuropathology Consortium. Analysis of  
 RNAs from the Brains of Individuals with Psychiatric  
 Diseases (Unpublished) Stanley Neuropathology Laboratory,  
 Johns Hopkins School of Medicine, Baltimore MD."

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Query Match      21.3%, 50.2% 103, EB 9; Length 436;
Best Local Similarity 84.6%, Pred. No. 2.2e-15;
Matches 115, Conserved 0, Mismatches 21, Indels 0, Gaps 0;

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RESULT 13	AW482601	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
	AW482601	405 bp	mRNA	linear	EST 09 JUL 2000		
	46248 MAF3	2P19	SUS	SC163	22NA.5',	mpna	sequence.
	AW482601						
	AW482601.1	71	7062707				
	EST.						
	PIG.						

ORGANISM  
Sus scrofa  
Euryptera, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
1 (bases 1 to 405)  
REFERENCE  
Falkenkrug, S. G., Fieking, R. A., Pohrer, G. A., Smith, T. P. L., Casan, F.,  
Althoff, S.

TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine  
 "Published" (2000)  
 COMMENT  
 CONTACT: Smith TPL  
 PROJECT: D. B. Barrett, G. B. Barrett

USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@meat1.mars.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 v1.99994.9. Vectors identified by cross\_match with the minscore 20  
 and -mismatch 12 options.  
 PCR Primers  
 FORWARD AGGAAATAGCTATGACCAT  
 REVERSE ATTTCGACGTGACGACG  
 Plate: 29 row: J column: 2  
 Seq primer: ATTTAGGTGACACTATAG.

FEATURES	Location/Qualifiers
source	1..405

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/organism="Sus scrofa"
/db_xref="taxon:9823"
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/tissue_type="focled"
/lab_host="PH10B"
/notes="Vaccines from SEPT6, Site 1, North Site 2: Saliv
Library made from pooled tissue from testis, ear,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      A1 a      120 c      138 g      66 t
ORIGIN

```

Query Match	19.34	Score 33.2	DB 10	Length 405
Best Local Similarity	79.74	Prod. No. 5.8e-13		
Matches 107	Conservative 0	Mismatches 20	Indels 0	Gaps 0

[illegible]

463 TATTTGATGCA TATAAAAGACAT ATCTCTGATATTT ATCTTTAAAGGGCAT 468  
|||||  
62 GGAATGATGCAATTAAGGGGAGATATTTTCTTCTATATTTGATATGAGGGGGCT 121  
|||||





1  
2  
3